STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/577,613					
Source:	TEWP					
Date Processed by STIC:	05/11/2006					
•						

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER:
ATTN: NEW RULES CASES:	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
1 Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - STIC Systems Branch - 03/02/06



IFWP

RAW SEQUENCE LISTING DATE: 05/11/2006
PATENT APPLICATION: US/10/577,613 TIME: 11:18:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577613.raw

3 <110> APPLICANT: Alexander, Cherkasky 5 <120> TITLE OF INVENTION: PCT/IB 2004/003536: CHERKASKY FUSION PROTEINS CONTAINING INTIBODY-ANTIGEN - AND MICROTUBULE - BINDING REGIONS AND IMMUNE RESPONSE - TRIGGERIND 6 Does Not Comply REGIONS Corrected Diskette Needed 9 <130> FILE REFERENCE: -Corrected Distriction

Corrected 12, 41

Consumer of the Holificial the Unknown. Pls Explains the Malerial of Source of Genetic Halerial Seed Heiser 11

In Ala Phe Tyr Gln Val Leu

15

19 Asn Gly Phe Ile Gln Ser
30

Son Val Leu Gly Glu Ala Lys
45

Dhe Asn Lys

Sheet -> 11 <140> CURRENT APPLICATION NUMBER: US/10/577,613 :--> 11 <141> CURRENT FILING DATE: 2006-04-28 11 <160> NUMBER OF SEQ ID NOS: 14 13 <170> SOFTWARE: PatentIn version 3.3 15 <210> SEQ ID NO: 1 16 <211> LENGTH: 676 17 <212> TYPE: PRT -> 18 <213> ORGANISM: (Artifical sequence -> 20 <220> FEATURE: -> 20 <223> OTHER INFORMATION: V--> 20 <400> 1 22 Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu 23 1 26 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser 27 20 25 30 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys 34 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys 35 55 38 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn 75 42 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser 95 43 46 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln 100 47 105 110 50 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe 115 120 54 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly 135 58 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu 59 145 155 150 160 62 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn 63 165 170 175 66 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu 180 185 70 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys 200 74 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/577,613

DATE: 05/11/2006

TIME: 11:18:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577613.raw

75		210					215					220				
			Ala	Gln	Ala	Pro				Asn	Aen		T.vc	Pro	Gly	lvs
	225	nsp	ALG	GIII	AIG	230	my 5	GIU	GIU	vob	235	Mon	Lys	1, 2 🗸	OL,	240
		y cz	Cly	Acn	Tuc	-	Gly	Tarc	Glu) en		y c n	Glar	Gly	Gly	_
83	Giu	wah	GLY	ASII	245		GIY	пуэ	GIU	250	Gry	ASII	Gry	Gry	255	Q ₁ y
	~3 v	Mot	Co~	Dro		•	7.00	Th~	Cor		Nan	120	λla	Dhe		ጥኮታ
87	GIA	MEL	Ser	260	FIIE	PIO	neu	TILL	265	MEC	ASP	гуз	ATO	270	Ile	1111
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	vaı	rea		nec	THE	PIO	val		GIA	IIIL	GIU	116	285	WOII	Tyr	ura
91	7 ~~	63.4	275 Mot	۳٦	71~	7707	T 011	280	C1 =	y an	T - 17	Ma see	_	7.110	y c w) co
	Asp	_	Mer	GTA	Arg	vат		Ald		ASD	AGT	300	MIG	гåа	Asp	VOII
95 98	LOU	290 Pro	Dro	Dha	Dro	712	295 Ser			N C YO	~ 1		בות	Val	Ara	Δla
		PIO	PIO	FILE	FIO			val	_	ASP	_	ıyı			Arg	320
	305 אות) Acr	, Cli	Dro		310				. Tle					בומי	-
		ı ASL	y Gry	PIL) WIG	Pile	: TTE			/ G10	1 261	. G1 1.	335	Gly
103		. <i>c</i> n-	n Dwe	. The	325			Mat	n n	330		. 17-3	Mat	· ሽምር		
		r GTI	1 PIC			1111	. val	. Met		_	, GII	ı vaı	. Me C	350		Thr
107		. (1).	. 37-	340		D		. ~1.	345		. או	1107	₹7 ~ 1			Glu
		GT.			116	PIC	Cys			ı Asp) Ale	ı vaı			l vai	Glu
111		. mb.	355 - 63		ተነ -	. 7	. 03	360				. The	365 		TOU	Clu
				r red	i iie	AIG			. Asī) (T)			ı Gıt	r Péa	Glu
115		370		Tou	11-1	~3 -	3·7·5				. ~1-	380		Nec	, Dro	Tle
	385		, 116	: rea	l val	390		HIG	PIC	, GIA	395		, 176	. WIG	, PLC	1le 400
			. New	Tla	Taco			. <i>(</i> 13.)		. 17-7			Tare	. Gla	, Thr	His
123		, urs	, war	, 116	405		, Gry	GIU	ı Cys	410		I WIC	пуз	, GI	415	
		G1.	, Dro	CAT			. G3.v	r T.au	T.A.			· Val	Gls	, Val		Glu
127		. Gly	ric	420		· IIC	. Gly	nen	425				. 013	430		
		Ġb	. Val			Phe	Pro	Val			Val	Met	Set			Asn
131			435					440			, , , ,		445			
		Leu			Pro	Glu	Asp			Lev	Pro	Glv			Arc	Asp
135		450				-	455	_				460				
				Ser	Thr	Leu			Thr	· Ile	Glr			Gly	Tyr	Pro
	465		J	,		470				•	479			•	•	480
			. Asn	Leu	Glv			Glv	Ast	Asn	Pro	Asp	Ast	Leu	ı Lev	Asn
143					485		•			490		•	•		495	
146	Ala	Lev	Asn	Glu	Gly	Ile	Ser	Ara	Ala	Asp	val	. Ile	: Ile	Thr	Ser	Gly
147				500	_				505	_				510		_
150	Gly	Val	Ser	Met	Gly	Glu	Lvs	Asp	Tyr	Leu	Lys	Gln	Val	Leu	a Asp	Ile
151	•		515		•		- •	520	_				525			
154	Asp	Leu	His	Ala	Gln	Ile	His	Phe	Gly	Arq	Val	Phe	Met	Lys	Pro	Gly.
155	-	530				•	535		- 3	ب -		540		•		- •
158	Leu	Pro	Thr	Thr	Phe	Ala	Thr	Leu	Asp	Ile	Asp	Gly	v Val	. Arc	Lys	Ile
	545					550			•	_	555				- -	560
162	Ile	Phe	Ala	Leu	Pro			Pro	Val	Ser			Val	Thr	Cys	Asn
163					565	_				570					5 7 5	
	Leu	Phe	Val	Val			Leu	Arq	Lys			Gly	Ile	. Leu	Asp	Pro
167				580					585			•		590		
170	Arg	Pro	Thr			Lys	Ala	Arg			Cys	Asp	Val	Lys	Leu	Asp
171	_		595			•		600			-	-	605	_		_

DATE: 05/11/2006

TIME: 11:18:49

```
PATENT APPLICATION: US/10/577,613
                    Input Set : A:\PTO.RJ.txt
                    Output Set: N:\CRF4\05112006\J577613.raw
    174 Pro Arg Pro Glu Tyr His Arg Cys Ile Leu Thr Trp His His Gln Glu
            610
    175
                                615
    178 Pro Leu Pro Trp Ala Gln Ser Thr Gly Asn Gln Met Ser Ser Arg Leu
    179 625
                            630
                                                 635
                                                                     640
    182 Met Ser Met Arg Ser Ala Asn Gly Leu Leu Met Leu Pro Pro Lys Thr
                                                                 655
                                             650
                        645
    183
    186 Glu Gln Tyr Val Glu Leu His Lys Gly Glu Val Val Asp Val Met Val
                                                             670
                                         665
    187
                    660
    190 Ile Gly Arg Leu
                675
    191
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N--> 199 <220> FEATURE:
N--> 199 <223> OTHER INFORMATION:
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    202 cttaaatgct gatcaacgca atggttttat ccaaagcctt aaagatgatc caagccaaag
                                                                               120
    204 tgctaacgtt ttaggtgaag ctaaaaaatt aaacgaatct caagcaccga aagctgacaa
                                                                               180
    206 caatttcaac aaagaacaac aaaatgcttt ctatgaaatc ttgaacatgc ctaacttgaa
                                                                               240
                                                                               300
    208 cgaagaacaa cgcaatggtt tcatccaaag cttaaaagat gacccaagtc aaagtgctaa
    210 cctattgtca gaagctaaaa agttaaatga atctcaagca ccgaaagcgg ataacaaatt
                                                                               360
    212 caacaaagaa caacaaaatg ctttctatga aatcttacat ttacctaact taaacgaaga
                                                                               420
                                                                               480
    214 acaacgcaat ggtttcatcc aaagcctaaa agatgaccca agccaaagcg ctaacctttt
    216 aqcagaagct aaaaagctaa atgatgcaca agcaccaaaa gctgacaaca aattcaacaa
                                                                               540
                                                                               600
    218 agaacaacaa aatgctttct atgaaatttt acatttacct aacttaactg aagagcaacg
                                                                               660
    220 taacggcttc atccaaagcc ttaaagacga tccttcagtg agcaaagaaa ttttagcaga
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                                                                               780
    224 agaagacggc aacaaacctg gcaaagaaga cggtaacggc ggcggcggcg gcgtttaggt
                                                                               840
    226 cacagtgctg tcgatatcac caaggtggct agaagacatc gcatgtctcc ttttcctctg
    228 acatctatgg acaaagcett tatcacagte etggagatga eteeggtget tgggacagaa
                                                                              960
    230 atcatcaatt accgagatgg aatggggcga gtccttgctc aagatgtata tgcaaaagac
                                                                             1020
    232 aatttacccc ccttcccagc atcagtaaaa gatggctatg ctgtccgagc tgctgatggc
                                                                             1080
    234 ccaggagate gtttcatcat tggggaatee caagetggtg aacagecaae tcagacagta
                                                                             1140
    236 atgccaggac aagtcatgcg ggttacaaca ggtgctccaa taccctgcgg tgctgatgca
                                                                             1200
    238 gtagtacaag tggaagatac cgaacttatc agggaatcag atgatggcac tgaagaactt
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    240 gaagtgcgaa ttctggtgca agctcggcca ggccaagata tcagacccat cggccatgac
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    242 attaaaagag gggaatgtgt tttggccaaa ggaacccaca tgggcccctc agagattggt
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                                                                             1440
    246 atgtcaacag ggaatgagct gctaaatcct gaagatgacc tcttaccagg gaagattcga
    248 gacagcaatc gttcaactct tctagcaaca attcaggaac atggttaccc cacgatcaac
                                                                             1500
                                                                             1560
    250 ttgggtattg taggagacaa cccagatgac ttactcaatg ccttgaatga gggtatcagt
                                                                             1620
    252 cgtgctgatg tcatcatcac atcagggggt gtatccatgg gggaaaagga ctatctcaag
                                                                             1680
    254 caggtgctgg acattgatct tcatgctcag atccattttg gcagggtttt tatgaaacca
                                                                             1740
    256 ggcttgccaa caacatttgc aactttggat attgatggtg taagaaaaat aatctttgca
                                                                             1800
    258 ctacctggga atcctgtatc ggctgtggtc acctgcaatc tctttgttgt gcctgcactg
                                                                             1860
    260 aggaaaatgc agggcatctt ggatcctcgg ccaaccatca tcaaagcaag gttatcatgt
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262 gatgtaaaac ttgatcctcg tccagaatac catcggtgta tactaacttg gcatcaccaa

RAW SEQUENCE LISTING

1920

RAW SEQUENCE LISTING DATE: 05/11/2006
PATENT APPLICATION: US/10/577,613 TIME: 11:18:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577613.raw

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264 gaaccactac cttgggcaca gagtacaggt aatcaaatga gcagccgtct gatgagcatg
                                                                              1980
                                                                              2040
    266 cgcagtgcca atggattgtt gatgctacct ccaaagacag aacagtacgt ggagctccac
    268 aaaggcgagg tggtggatgt catggtcatt ggacggctat gatggtcacc ag
                                                                              2092
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    273 <212> TYPE: PRT
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2--> 274 <213> ORGANISM: (Artifical sequence
    277 <220> FEATURE:
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    279 <222> LOCATION: (264)..(264)
    280 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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    283 <221> NAME/KEY: misc_feature
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    288 <221> NAME/KEY: misc feature
    289 <222> LOCATION: (281)..(281)
    290 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
    292 <400> SEQUENCE: 3
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                                                                  15
    295 1
                        5
                                             10
    298 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser
    299
    302 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys
                35
                                     40
    303
    306 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys
                                                     60
    307
            50
                                55
    310 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
                            70
                                                 75
    311 65
    314 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
    318 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
                    100
    319
                                         105
    322 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
    323
                115
                                     120
                                                         125
    326 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
    327
            130
                                135
    330 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
    331 145
                            150
                                                 155
    334 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
    335
                        165
                                             170
    338 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
    339
                                                             190
                    180
                                         185
    342 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
    343
                195
                                     200
                                                         205
    346 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
    347
            210
                                215
                                                     220
    350 Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
```

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TIME: 11:18:49

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Input Set : A:\PTO.RJ.txt
                     Output Set: N:\CRF4\05112006\J577613.raw
                             230
                                                  235
                                                                       240
     351 225
     354 Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly Gly Gly
                                              250
                         245
     355
W--> 358 Gly Ala Ala Ala Ser Thr Ala Xaa Ala Ser Thr Ala Lys Glu Thr Ala
                                                              270
     359
                                          265
                     260
W--> 362 Glu Ala Val Ala Asp Xaa Ile Leu Xaa Lys Ala Gly Pro Leu Val Ala
                                                          285
                 275
                                     280
     363
     366 Val Ser Ala Val Ala Leu Asp Ile Thr Ala Tyr Pro
     367
             290
                                 295
                                                    7 Same Error
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     371 <211> LENGTH: 912
     372 <212> TYPE: DNA
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     377 <221> NAME/KEY: misc_feature
     378 <222> LOCATION: (792)..(792)
     379 <223> OTHER INFORMATION: n is a, c, g, t or u
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     382 <221> NAME/KEY: misc feature
     383 <222> LOCATION: (835)..(835)
     384 <223> OTHER INFORMATION: n is a, c, g, t or u
     386 <220> FEATURE:
     387 <221> NAME/KEY: misc feature
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     391 <400> SEQUENCE: 4
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                                                                                 60
                                                                                120
     394 cttaaatgct gatcaacgca atggttttat ccaaagcctt aaagatgatc caagccaaag
     396 tgctaacgtt ttaggtgaag ctaaaaaatt aaacgaatct caagcaccga aagctgacaa
                                                                                180
                                                                                240
     398 caatttcaac aaagaacaac aaaatgcttt ctatgaaatc ttgaacatgc ctaacttgaa
     400 cgaagaacaa cgcaatggtt tcatccaaag cttaaaagat gacccaagtc aaagtgctaa
                                                                                300
                                                                                360
     402 cctattgtca qaaqctaaaa aqttaaatga atctcaagca ccgaaagcgg ataacaaatt
     404 caacaaagaa caacaaaatg ctttctatga aatcttacat ttacctaact taaacgaaga
                                                                                420
                                                                                480
     406 acaacgcaat ggtttcatcc aaagcctaaa agatgaccca agccaaagcg ctaacctttt
     408 agcagaagct aaaaagctaa atgatgcaca agcaccaaaa gctgacaaca aattcaacaa
                                                                                540
                                                                                600
     410 agaacaacaa aatgctttct atgaaatttt acatttacct aacttaactg aagagcaacg
                                                                                660
     412 taacggcttc atccaaagcc ttaaagacga tccttcagtg agcaaagaaa ttttagcaga
                                                                                720
     414 agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa gacaacaaca aacctggtaa
                                                                                780
     416 agaagacggc aacaaacctg gcaaagaaga cggtaacggc ggcggcggcg gcgcggccgc
                                                                                840
W--> 418 gtcgaccgcg gncgcgtcga cggcaaagga gactgctgag gctgttgctg atganatact
                                                                                900
W--> 420 gganaagget gggccacttg ttgctgtgtc tgctgttgca cttgatataa ctgcctaccc
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     422 ctaaaagcca aa
     425 <210> SEQ ID NO: 5
                                                        Same Error
     426 <211> LENGTH: 3718
     427 <212> TYPE: DNA
C--> 428 <213> ORGANISM: (Artifical sequence
W--> 430 <220> FEATURE:
W--> 430 <223> OTHER INFORMATION:
W--> 430 < 400 > 5
                                                      The type of errors shown exist throughout
                                                     the Sequence Listing. Please check subsequent
                                                          sequences for similar errors.
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/577,613

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/11/2006 PATENT APPLICATION: US/10/577,613 TIME: 11:18:50

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577613.raw

Please Note:

Jse of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 264,278,291
Seq#:4; N Pos. 792,835,844
Seq#:8; N Pos. 488,531,540
Seq#:9; N Pos. 440,483,492
Seq#:12; N Pos. 792,835,844

Jse of <220> Peature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Jse of <220> to <223> is MANDATORY if <R13> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,5,6,7,10,11,13,14

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/577,613

DATE: 05/11/2006
TIME: 11:18:50

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577613.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:18 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1 L:20 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213> ORGANISM: Artificial Sequence L:20 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213> ORGANISM: Artificial Sequence L:20 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1, Line#:20 L:197 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2 L:199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213> ORGANISM: Artificial Sequence L:199 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213> ORGANISM: Artificial Sequence L:199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2, Line#:199 L:274 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3 L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:256 L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:272 L:373 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4 L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:780 L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:840 L:428 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5 L:430 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213> ORGANISM: Artificial Sequence L:430 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213> ORGANISM: Artificial Sequence L:430 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5, Line#:430 L:559 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6 L:561 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213> ORGANISM: Artificial Sequence L:561 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213> ORGANISM: Artificial Sequence L:561 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6, Line#:561 L:652 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7 L:654 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213> ORGANISM: Artificial Sequence L:654 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213> ORGANISM: Artificial Sequence L:654 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7, Line#:654 L:743 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8 L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:480 L:812 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9 L:845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420 L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:480 L:881 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10 L:883 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213> ORGANISM: Artificial Sequence L:883 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213> ORGANISM: Artificial Sequence L:883 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10, Line#:883 L:1028 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11 L:1030 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213> ORGANISM: Artificial Sequence

L:1030 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>

ORGANISM: Artificial Sequence

L:1030 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11, Line#:1030

L:1173 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12

L:1218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:780

L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:840

L:1252 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13

L:1254 M:258 W: Mandatory Feature missing, <220> Tag not found for SBQ#:13, <213>

ORGANISM: Artificial Sequence

L:1254 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>

ORGANISM: Artificial Sequence

L:1254 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13, Line#:1254

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/577,613
DATE: 05/11/2006
TIME: 11:18:50

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRP4\05112006\J577613.raw

L:1355 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14 L:1357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>

ORGANISM: Artificial Sequence

L:1357 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>

ORGANISM: Artificial Sequence

L:1357 M:258 W: Mandatory Peature missing, <223> Blank for SBQ#:14, Line#:1357